

Sequence Alignments

RESULT 6

HUMTNFRP 2136 bp mRNA linear PRI 03-AUG-1993
 LOCUS Homo sapiens (clone CD18) tumor necrosis factor receptor 2 related
 DEFINITION protein mRNA, complete cds.
 ACCESSION L04270.1 GI:339761
 VERSION 1
 KEYWORDS tumor necrosis factor receptor 2 related protein.
 SOURCE Homo sapiens (library: liver cDNA of P.M.) liver cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2136)
 AUTHORS Baens, M., Chaffanet, M., Cassiman, J.J., van den Berghe, H. and Marynen, P.
 TITLE Construction and evaluation of a hcdNA library of human 12p
 transcribed sequences derived from a somatic cell hybrid
 JOURNAL Genomics 16 (1), 214-218 (1993)
 MEDLINE 93252381
 PUBMED 8486360
 FEATURES
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
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 /tissue_lib="liver cDNA of P.M."
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 /note="putative"
 /codon_start=1
 /product="tumor necrosis factor receptor 2 related protein"
 /protein_id="AAA36757.1"
 /db_xref="GI:339762"
 /translation="MLPWTASPLANGPLVGLFGLLAASOPAVPPYASENOTCR
 DOEKEYFEFRIACSCPPGIVYSAKRSINDVTCARCAENSNEHNLYITICOLCR
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 GKNHNCVPCAKHPQNTSSPARGCPHTRCNGLVEAPAGTQSDTCKNPLEPLP
 PEMSTMLVALLPLAFELLATVFSICLWKSHPSLRRPQGGEPVAG
 SHEPKAHYFEPDLVQPLLPISDVSVPSTGLPAAPVLEAGVPOQSQPLDLTREPQLE
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 DPGPFLSTPHQEDGKAWHLAETEHCGATPSNRGNQFIHID"

CDS

BASE COUNT 446 a 706 c 608 g 376 t
 ORIGIN
 Query Match 91.3%; Score 1809.2; DB 9; Length 2136;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 1929; Conservative 0; Mismatches 3; Indels 108; Gaps 1;

QY 51 GCCCTGGAGCCGCGCTGCGCTCCCGCGCTCGGGTGCACATCGGCCCTGAGTCCG 110
 Db 1 GCCCTGGAGCCGCGCTGCGCTCCCGCGCTCGGGTGCACATCGGCCCTGAGTCCG 60
 QY 111 TCCAGGCTTGGCTCGGGCAGCCGCGCACCGCTGCGGAGAGTGGGGCTCTGTC 170
 Db 61 TCCAGGCTTGGCTCGGGCAGCCGCGCACCGCTGCGGAGAGTGGGGCTCTGTC 120
 QY 171 CTTCTCCAGGCCCCACAGTTGTGCGCGCTGCGGAGTGGCGCATCTCTGCT 230
 Db 121 CTTCTCCAGGCCCCACAGTTGTGCGCGCTGCGGAGTGGCGCATCTCTGCT 180
 QY 231 TGGCCACCTCTGCCCCCGGCTGCGCTGGGGGCTCTGTGCTGGGGCTCTTGGGGT 290
 Db 181 TGGCCACCTCTGCCCCCGGCTGCGCTGGGGGCTCTGTGCTGGGGCTCTTGGGGT 240

291 CTGGAGCATCGCAGCCCCAGCGGTGCTCCATATGCTCGGAGAACACAGACCTGCAGG 350
 Db 241 CTGGCAGCATCGCAGCCCCAGCGGTGCTCCATATGCTCGGAGAACACAGACCTGCAGG 300
 QY 351 GACCAGGAAAAGGAATACTATGAGCCCCAGACCCGATCTGCTGCTCCGCTGCCGCCA 410
 Db 301 GACCAGGAAAAGGAATACTATGAGCCCCAGACCCGATCTGCTGCTCCGCTGCCGCCA 360
 QY 411 GGCACCTATGCTCAGCTAAATGATAGCGCATCCGGGACACAGTTTGTGCCACATGTGC 470
 Db 361 GGCACCTATGCTCAGCTAAATGATAGCGCATCCGGGACACAGTTTGTGCCACATGTGC 420
 QY 471 GAGATTCCTACAGCAGCAGCTGGAACCTGACCATCTGCCAGCTGTGCCGCCCTGT 530
 Db 421 GAGATTCCTACAGCAGCAGCTGGAACCTGACCATCTGCCAGCTGTGCCGCCCTGT 480
 QY 531 GACCCAGTGTATGGCCCTCGAGGAGATTGCCCTCGACAAAGCAAGAGAGAGAGAGTGC 590
 Db 481 GACCCAGTGTATGGCCCTCGAGGAGATTGCCCTCGACAAAGCAAGAGAGAGAGTGC 540
 QY 591 CGCTGCGAGCCGGAATGTTCTGCTGCTGGGCCCTCGAGTGTACACACTCGGAGCTA 650
 Db 541 CGCTGCGAGCCGGAATGTTCTGCTGCTGGGCCCTCGAGTGTACACACTCGGAGCTA 600
 QY 651 CTTTCTGACTGCCCCCTGCGACTGAGCGGAGCTCAAAAGATGAAGTTGGGAAGGTTAAC 710
 Db 601 CTTTCTGACTGCCCCCTGCGACTGAGCGGAGCTCAAAAGATGAAGTTGGGAAGGTTAAC 660
 QY 711 AACCACTGCGTCCCTGCAAGGAGGAGCTTCCAGATACTCTCCCTCCCGAGCGCCGC 770
 Db 661 AACCACTGCGTCCCTGCAAGGAGGAGCTTCCAGATACTCTCCCTCCCGAGCGCCGC 720
 QY 771 TGCCAGCCCCACACAGGCTGTGAGAACCAAGTGTGTGGAGGAGCTCCAGGCACTGCC 830
 Db 721 TGCCAGCCCCACACAGGCTGTGAGAACCAAGTGTGTGGAGGAGCTCCAGGCACTGCC 780
 QY 831 CAGTCCGACACAACTGCAAAAATCCATTAGAGCACTGCCGCCCGAGAGATGCA 884
 Db 781 CAGTCCGACACAACTGCAAAAATCCATTAGAGCACTGCCGCCCGAGAGATGCA 840
 QY 885 ----- 884
 Db 841 ATGCTGATGTGGCGGTCTGCTGCCACTGGCTTCTTCTGCTCTTGGCCACCTGCTTC 900
 QY 885 -----GGATCGCTGCTCAAGAGG 902
 Db 901 TCTGCTATCTGGAAGCCACCCCTTCTCTCTCAGGAAACTGGGATCGCTGCTCAAGAGG 960
 QY 903 CGTCCGAGGAGAGGAGGACCCAACTCTCTGCTGAGCTGGAAGCTGGAGCTCCGAAGGCCAT 962
 Db 961 CGTCCGAGGAGAGGAGGACCCAACTCTGCTGAGCTGGAAGCTGGAGCTCCGAAGGCCAT 1020
 QY 963 CCATACTTCCCTGACTTGTGTACAGCCACTGTACCCATTTCTGGAGATGTTTCCCCAGTA 1022
 Db 1021 CCATACTTCCCTGACTTGTGTACAGCCACTGTACCCATTTCTGGAGATGTTTCCCCAGTA 1080
 QY 1023 TCCACTGGGCTCCCGCAGCCCCAGTTTGGAGGAGGAGGCTCCGCAACAGAGAGTCT 1082
 Db 1081 TCCACTGGGCTCCCGCAGCCCCAGTTTGGAGGAGGAGGCTCCGCAACAGAGAGTCT 1140
 QY 1083 CTGGACTTGACAGGAGCGCAGTTGGAAACCCGGGAGCAGAGCAGGTTGCCACAGGT 1142
 Db 1141 CTGGACTTGACAGGAGCGCAGTTGGAAACCCGGGAGCAGAGCAGGTTGCCACAGGT 1200
 QY 1143 ACCAATGGGATTCATGTCACCGCGGTCTATGACTATCTACTGCAACATCTACATCTAC 1202
 Db 1201 ACCAATGGGATTCATGTCACCGCGGTCTATGACTATCTACTGCAACATCTACATCTAC 1260
 QY 1203 AATGGACCACTACTTGGGGGAGCACCAGGCTCTGGAGACCTTCCAGCTACCCCGAACCT 1262
 Db 1261 AATGGACCACTACTTGGGGGAGCACCAGGCTCTGGAGACCTTCCAGCTACCCCGAACCT 1320

1263 CCATACCCCATTTCCGAAGAGGGGACCCCTGGCCCTCCGGGCTCTACACCCACCAG 1322
 QY
 1321 CCATACCCCATTTCCGAAGAGGGGACCCCTGGCCCTCCGGGCTCTACACCCACCAG 1380
 Db
 1323 GAAGATGGCAAGGCTTGGCACCTTAGCGGACAGACACTGTGTGTCACACCCCTCTAAC 1382
 QY
 1381 GAAGATGGCAAGGCTTGGCACCTTAGCGGACAGACACTGTGTGTCACACCCCTCTAAC 1440
 Db
 1383 AGGGGCCCAAGGACCAATTTATCACCCATGACTGACTGTGATGTGAGAAAAGGAGAGA 1442
 QY
 1441 AGGGGCCCAAGGACCAATTTATCACCCATGACTGACTGTGATGTGAGAAAAGGAGAGA 1500
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 1443 AGGGGGCACAAAGGGACCTTCTCCCTTGAGGCTGCCCTGCCACGTGGGATTCACAGGG 1502
 QY
 1501 AGGGGGCACAAAGGGACCTTCTCCCTTGAGGCTGCCCTGCCACGTGGGATTCACAGGG 1560
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 1503 GCCTGAGTAGGGCCCGGGAGAGCAGAGCCCTAAGGATTAAGGCTTCAGACACCTCTGAGA 1562
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 1561 GCCTGAGTAGGGCCCGGGAGAGCAGAGCCCTAAGGATTAAGGCTTCAGACACCTCTGAGA 1620
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 1623 ACCTGAGGCTCCCGGACAGCCACCCACCCCTGGGGCTGCTCAGCCTCAGGCACGGAC 1682
 QY
 1681 ACCTGAGGCTCCCGGACAGCCACCCACCCCTGGGGCTGCTCAGCCTCAGGCACGGAC 1740
 Db
 1683 AGGGACATGATACCAACTGCTGCCACTACAGCAGCGGACCCGGAGCAGCGCACCCGAG 1742
 QY
 1741 AGGGACATGATACCAACTGCTGCCACTACAGCAGCGGACCCGGAGCAGCGCACCCGAG 1800
 Db
 1743 GGAGCGCCACACGGTCACTGCAAGGACGTACGGGCCCTCTAAAGGATTCGTGGTGC 1802
 QY
 1801 GGAGCGCCACACGGTCACTGCAAGGACGTACGGGCCCTCTAAAGGATTCGTGGTGC 1860
 Db
 1803 TCATCCCAAGCTTCAGAGACCCCTTTGGGGTTCCACACTTCACGTGACTGAGTAGACC 1862
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 1861 TCATCCCAAGCTTCAGAGACCCCTTTGGGGTTCCACACTTCACGTGACTGAGTAGACC 1920
 Db
 1863 CTGCATGAGATGAATATATAGGAGGACGCTCCTTCCTCCCTCCCTCCTAGAGAGAGAA 1922
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 1921 CTGCATGAGATGAATATATAGGAGGACGCTCCTTCCTCCCTCCCTCCTAGAGAGAGAA 1980
 Db
 1923 AGGGAGTCATTAAACAACCTAGGGGTTGGGTAGGATTCCTAGGTATGGGAGAGTTTGG 1982
 QY
 1981 AGGGAGTCATTAAACAACCTAGGGGTTGGGTAGGATTCCTAGGTATGGGAGAGTTTGG 2040
 Db

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DR EMBL; L04270; AAA36757.1; -
DR EMBL; BC026262; AAH26262.1; -
DR HSSP; P25942; ICDF.
DR Genew; HGNC:6718; LTR.
DR MIM; 600979; -
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD00071; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 3.
DR Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 435 TUMOR NECROSIS FACTOR RECEPTOR
FT DOMAIN 31 227 SUPERFAMILY MEMBER 3.
FT TRANSMEM 228 248 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 249 435 POTENTIAL.
FT REPEAT 42 81 CYTOPLASMIC (POTENTIAL).
FT REPEAT 82 124 TNFR-CYS 1.
FT REPEAT 125 168 TNFR-CYS 2.
FT REPEAT 169 211 TNFR-CYS 3.
FT DISULFID 43 58 TNFR-CYS 4.
FT DISULFID 59 72 BY SIMILARITY.
FT DISULFID 62 80 BY SIMILARITY.
FT DISULFID 83 98 BY SIMILARITY.
FT DISULFID 101 116 BY SIMILARITY.
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FT DISULFID 139 148 BY SIMILARITY.
FT DISULFID 142 167 BY SIMILARITY.
FT DISULFID 170 185 BY SIMILARITY.
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FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 435 AA; 46709 MW; 62462656022F656F CRC64;

Query Match 98.8%; Score 2220; DB 1; Length 435;
Best Local Similarity 91.7%; Pred. No. 7.1e-120;
Matches 399; Conservative 0; Mismatches 0; Indels 36; Gaps 1;
QY 1 MLFWATSAFLWGLVGLGLAASQVAVPPYASENQTCRDOKEYEPOHRIICCS 60
DB 1 MLFWATSAFLWGLVGLGLAASQVAVPPYASENQTCRDOKEYEPOHRIICCS 60
QY 61 RCPPTVTSKRSIRDTVCATCAENSNEHNYLTTCQLCRPCDPVNGLEETAPCTSKR 120
DB 61 RCPPTVTSKRSIRDTVCATCAENSNEHNYLTTCQLCRPCDPVNGLEETAPCTSKR 120
QY 121 KTCRCOPGMECAAWALECTHCELLSDCPGTEAELDEKGVGNHCVCKAGHFQNTSS 180
DB 121 KTCRCOPGMECAAWALECTHCELLSDCPGTEAELDEKGVGNHCVCKAGHFQNTSS 180
QY 181 PSARCQPHTRCENGLVEAAGPTAQSDTTCNPLEPLPEPMS. 222
DB 181 PSARCQPHTRCENGLVEAAGPTAQSDTTCNPLEPLPEPMS. 222
QY 223 -----GSLKRRPQEGNPNVAGSWEPKHAHPYDPLVQPLPISGD 264
DB 241 ATVFSCIWKSHPSLCRKLGLSKRRPQEGNPNVAGSWEPKHAHPYDPLVQPLPISGD 300
QY 265 VSPVSTGLPAAPVLEAGVPOOGLDTRPQLRPGEOQVAGHTNGIHVGGSMITGN 324
DB 301 VSPVSTGLPAAPVLEAGVPOOGLDTRPQLRPGEOQVAGHTNGIHVGGSMITGN 360
QY 325 IYIYNGPVLGPPGPGDLPATPEPPYPIPEGDPGPPGLSTPHQEDGKAWHAEHCGA 384
DB 361 IYIYNGPVLGPPGPGDLPATPEPPYPIPEGDPGPPGLSTPHQEDGKAWHAEHCGA 420
QY 385 TPSNRGPRNQIFTHD 399
DB 421 TPSNRGPRNQIFTHD 435

RESULT 1
TNFR3_HUMAN STANDARD; PRT; 435 AA.
ID P36941;
AC 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 3 precursor
DE (Lymphotoxin-beta receptor) (Tumor necrosis factor receptor).
DE protein) (Tumor necrosis factor C receptor).
GN LTR OR TNFRSF3 OR TNFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RT TISSUE=Liver;
MEDLINE=93252381; PubMed=8486360;
RA Baens M., Chafanet M., Cassiman J.J., den Berghe H., Marynen P.;
RT "Construction and evaluation of a hncDNA library of human l2p
RL transcribed sequences derived from a somatic cell hybrid.";
RL Genomics 16:214-218(1993).
[2]
RS SEQUENCE FROM N.A.
RT TISSUE=Lung;
Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
[3]
RS MEDLINE=94225209; PubMed=8171323;
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RT "A lymphotoxin-beta-specific receptor.";
RL Science 264:707-710(1994).
[4]
RS CHARACTERIZATION
MEDLINE=99223511; PubMed=10207006;
RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
RL death in HeLa cells.";
RL J. Biol. Chem. 274:11868-11873(1999).
[5]
RS FUNCTION.
MEDLINE=20261554; PubMed=10799510;
RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
RA Whitebeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
RT "The lymphotoxin-beta receptor is necessary and sufficient for
RL LIGHT-mediated apoptosis of tumor cells.";
RL J. Biol. Chem. 275:14307-14315(2000).
CC -!- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
CC and TRAF5. May play a role in the development of lymphoid organs.
CC -!- SUBUNIT: Self-associates.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

QY 1 MLFWATSAFLWGLVGLGLAASQVAVPPYASENQTCRDOKEYEPOHRIICCS 60
DB 1 MLFWATSAFLWGLVGLGLAASQVAVPPYASENQTCRDOKEYEPOHRIICCS 60
QY 61 RCPPTVTSKRSIRDTVCATCAENSNEHNYLTTCQLCRPCDPVNGLEETAPCTSKR 120
DB 61 RCPPTVTSKRSIRDTVCATCAENSNEHNYLTTCQLCRPCDPVNGLEETAPCTSKR 120
QY 121 KTCRCOPGMECAAWALECTHCELLSDCPGTEAELDEKGVGNHCVCKAGHFQNTSS 180
DB 121 KTCRCOPGMECAAWALECTHCELLSDCPGTEAELDEKGVGNHCVCKAGHFQNTSS 180
QY 181 PSARCQPHTRCENGLVEAAGPTAQSDTTCNPLEPLPEPMS. 222
DB 181 PSARCQPHTRCENGLVEAAGPTAQSDTTCNPLEPLPEPMS. 222
QY 223 -----GSLKRRPQEGNPNVAGSWEPKHAHPYDPLVQPLPISGD 264
DB 241 ATVFSCIWKSHPSLCRKLGLSKRRPQEGNPNVAGSWEPKHAHPYDPLVQPLPISGD 300
QY 265 VSPVSTGLPAAPVLEAGVPOOGLDTRPQLRPGEOQVAGHTNGIHVGGSMITGN 324
DB 301 VSPVSTGLPAAPVLEAGVPOOGLDTRPQLRPGEOQVAGHTNGIHVGGSMITGN 360
QY 325 IYIYNGPVLGPPGPGDLPATPEPPYPIPEGDPGPPGLSTPHQEDGKAWHAEHCGA 384
DB 361 IYIYNGPVLGPPGPGDLPATPEPPYPIPEGDPGPPGLSTPHQEDGKAWHAEHCGA 420
QY 385 TPSNRGPRNQIFTHD 399
DB 421 TPSNRGPRNQIFTHD 435